



125

**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82) EcoNI (96)

101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)** 201 **Psp1406I (203)** GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGCC EcoNI (287) **Bsu36I (291)**

301 **GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC**

401 **GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT** NgoMIV (441) NaeI (441)

501 **TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCAACATGTTACCGACCAAGCTGGGGCCGCGCGGCTCTGGG** AgeI (552) BspLU11I (560) SacII (584) XmaI (694)

601 **13> R G S A L G G S L N R T P T G R P G G G G G T R G A N G G R V P G** SandI (689)

701 **47> N G A G L G P G R L E R E A A A A A A T T P A P T A G A L Y S G S** SacII (773)

801 **80> E G D S E S G E E E L G A E R R G L K R S L S E M E I G M V V G G** BsaBI (873)

901 **113> P E A S A A A T G G Y G P V S G A V S G A K P G K K T R G R V K I** XmaI (980)

1001 **147> K M E F I D N K L R R Y T T F S K R K T G I M K K A Y E L S T L T** StuI (1073)

1101 **180> G T Q V L L L V A S E T G H V Y T F A T R K L Q P M I T S E T G K A** Bst1107I (1143) PstI (1165)

1201 **213> L I Q T C L N S P D S P P R S D P T T D Q R M S A T G F E E T D L** BglIII (1293)

1301 **247> T Y Q V S E S D S S G E T K D T L K P A F T V T N L P G T T S T I** NgoMIV (1353) NaeI (1353)

1401 **280> Q T A P S T S T T M Q V S S G P S F P I T N Y L A P V S A S V S P S**

1501 **313> A V S S A N G T V L K S T G S G P V S S G G L M Q L P T S F T L M** PvuII (1573) ApaLI (1645)

1601 **347> P G G A V A Q Q V P V Q A I Q V H Q A P Q Q A S P S R D S S T D L**

1701 **380> T Q T S S S G T V T L P A T I M T S S V P T T V G G H M M Y P S P H** SphI (1797)

1801 **413> A V M Y A P T S G L G D G S L T V L N A F S Q A P S T M Q V S H S** XcmI (1817) XmnI (1854)

1901 **447> Q V Q E P G G V P Q V F L T A S S G T V Q I P V S A V Q L H Q M A** XcmI (1905)

2001 **480> V I G Q Q A G S S S N L T E L Q V V N L D T A H S T K S E •** NheI (2096)

2101 **GCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGC**

2201 **TTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAAATTGCATTCATTTTATGTTTCAGGTTACGGGGAGGTGGGAGGTTTTTTAA** HpaI (2234) MfeI (2245)

2301 **AGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCATAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGG** EcoRI (2330)

2401 GATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGATTTTCCCA

2501 AGGTTTGAAC TAGCTCTTTCATTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTT TAGTAAAATATTCAGAAATAATTTAAATACATCATTG  
SspI (2569) SwaI (2583)

2601 CAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCT

2701 TTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCA  
141 • N R T Y K L P I L E E I T T K V L K G  
SacI (2844)

2801 TTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGTGACCACCCTGATGGATCTGTCCACCTCAT  
120 N M E I L V F C D P A Y D S I L E R C M G C P S V V R I S R D V E D

2901 CAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCT  
87 S Y P H R V A V I T D F D K Q G N S V A S G I A I A E A C V T V R  
StuI (3008)

3001 GCCAATGTAGGCCCAATGTGGACAGCAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGCTCATAGAGCATGGTG  
54 G I Y A E I H V A S I I E G T K T R I A A G V H H K N D E Y L M T  
XmnI (3150)

3101 ATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGATTATACATATGCGG  
20 I K E T A V E V L E L D Q Q S I N F T K M  
SacI (3273)

3201 ATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTATCTGACGGTTCACAAACGAGCTCTGCTTATATAGACCTCCACC  
AseI (3216)

3301 GTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGT  
SpeI (3371)

3400 CAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAA

SnaBI (3499)

3500 TACGTAGATGTA CTGCAAGTAGGAAAGTCCATAAGT CATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTA

NdeI (3604)

3600 CTTGGCATATGATACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGG

PstI (3783)

3700 GAACATACGTCATTATTGACGTCAATGGGCGGGGTGCTTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTG CAG G TT AA TTA  
SdaI (3782) PacI (3790)

BspLU11I (3800)

3798 AGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACA  
3898 AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATAACAGGCGTTTTCCCTGGAAAGTCCCTCGTGCCTCTCTGTTCCGACC  
3998 CTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT

ApaLI (4114)

4098 GCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTGAGCCGACCGTGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTT  
4198 ATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACT  
4298 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA AAAAGATTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTAGCG  
4398 GTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGA

PacI (4530) SwaI (4539) NotI (4549)

4498 AAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGT  
4598 TTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAACAAACGAAACAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGACAGGTGCCAG  
4698 AACATTTCTCTATCGAA